This presentation does not contain any proprietary, confidential, or otherwise restricted information



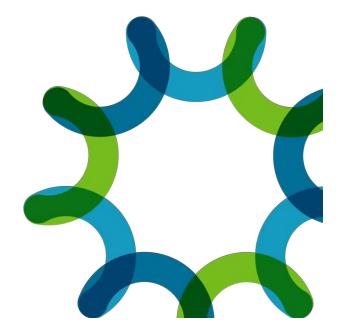


ABF Overview

Nathan J. Hillson

Principal Investigator

BETO Peer Review 2019 Conversion Technologies 8:40-9:30AM March 7, 2019 Denver, CO



Goal Statement

 Goal: Enable biorefineries to achieve 50% reductions in time to bioprocess scale-up as compared to the current average of around 10 years by establishing a distributed Agile BioFoundry that will productionize synthetic biology.



 Outcomes: 10X improvement in Design-Build-Test-Learn cycle efficiency, new host organisms, new IP and manufacturing technologies effectively translated to U.S. industry ensuring market transformation.



 Relevance: Public infrastructure investment that increases U.S. industrial competitiveness and enables new opportunities for private sector growth and jobs.







Quad Chart Overview

Timeline

- Start: October 1, 2016
- End: September 30, 2019
- 83% complete

Budget

	Total Costs Pre FY17	FY17 Costs	FY18 Costs	Total Planned Funding (FY19- Project End Date)
DOE Funded	\$2.1M	\$9.2M	\$13.8M	\$18.2M

Partners: LBNL (24%); PNNL (19%); SNL (19%); NREL (18%); LANL (8%); ORNL (7%); ANL (5%); INL (0.5%)

Barriers

- Ct-D. Advanced Bioprocess Development
- Ct-L. Decreasing Development Time for Industrially Relevant Microorganisms
- ADO-D. Technology Uncertainty of Integration and Scaling
- At-E. Quantification of Economic, Environmental, and Other Benefits/Costs

Objective

Enable biorefineries to achieve 50% reductions in time to bioprocess scale-up.

End of Project Goals

Demonstrate target/host pair production of at least 3 molecules at 10 g/L, 100 mg/L/hr, at 40% of theoretical yield from DMR-EH at 10 L. Demonstrate value of non-intuitive Learn predictions.





1 - Project Overview





The Opportunity

The U.S. has ~billion tons of renewable biomass available annually that is a strategic national resource for the bioeconomy

U.S. bioeconomy is estimated at ~\$250B/yr and expected to grow significantly over the next decade



Mobilizing and valorizing this resource through biomanufacturing could rapidly expand the U.S. bioeconomy

Biomanufacturing remains nascent in terms of robustness, scale and standardization





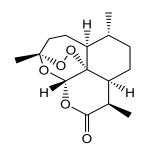
The Challenge: Cost and Time to Market

Molecule Company Cost Time

1,3-Propanediol DuPont - \$120M 15 years

(PDO) Tate & Lyle

Artemisinin



UC Berkeley, Amyris,

Sanofi

\$50M

10 years

Possible savings of *billions* of dollars by reducing development time of products





Public Infrastructure Investment Enables Private Industry

Public investment in biomanufacturing infrastructure

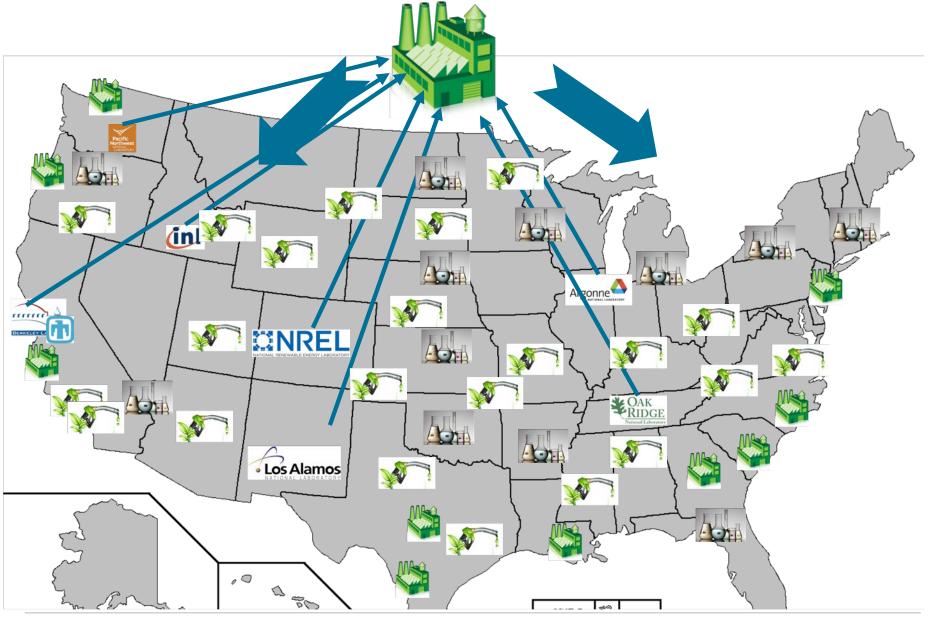
Private investment in product development, scaling, and tailoring to unique pathways and products

Adapted from Lyft





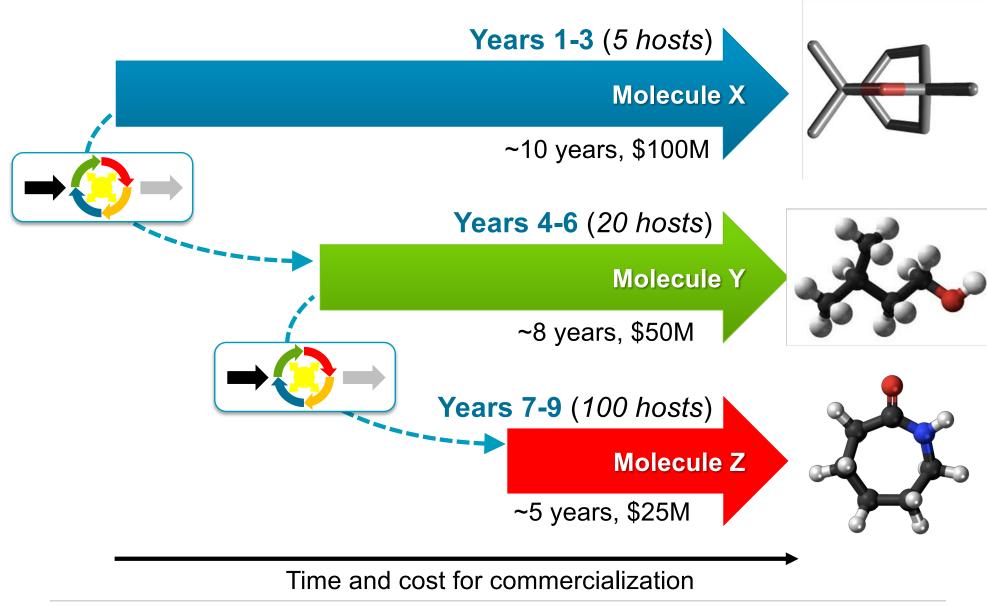
A Distributed Agile BioFoundry







Agile BioFoundry Will Reduce Time-to-Scale up







2 – Approach (Management)





Agile BioFoundry Project Structure

- Funding: planned at \$41.2M over 3 years (FY17-19)
 - Year 1 (FY17): \$9.2M
 - Year 2 (FY18): \$13.6M
 - Year 3 (FY19): \$15.7M
 - DFO funding: \$2.7M
- Coordination with BEEPS FOA
- Eight National Lab consortium
- Industrial Advisory Board actively engaged
- Six tasks for overall project
 - 4 research tasks, 2 management tasks
- One milestone per quarter
 - Annual SMART milestone
 - 18 and 36 month Go/No-Go decision points
- Monthly and quarterly progress reporting to BETO





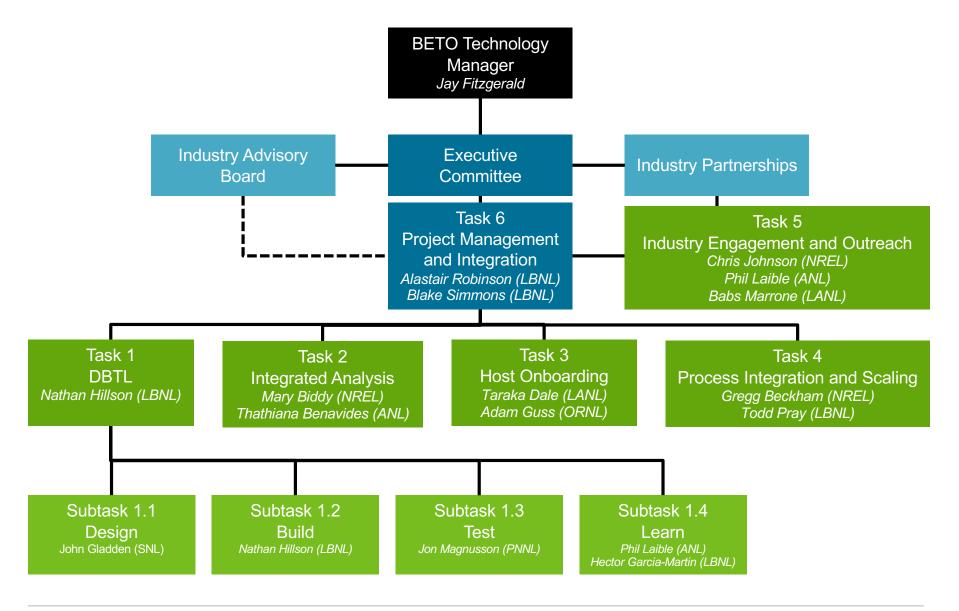
Six Tasks for Overall Project

- Task 1: Design-Build-Test-Learn (Nathan Hillson lead)
 - Integrate design-build-test-learn cycle with process automation and sample tracking.
- Task 2: Integrated Analysis (*Mary Biddy/Thathiana Benavides* co-leads)
 - Evaluate proposed molecules; develop, update, and improve existing process designs and LCA.
- Task 3: Host Onboarding (Taraka Dale/Adam Guss co-leads)
 - Evaluate possible host organisms to determine which on-boarding criteria are not yet met, and fill these gaps through tool development and data collection.
- Task 4: Process Integration and Scale-up (*Gregg Beckham/Todd Pray* co-leads)
 - Standardize, produce, ship, and store hydrolysates; compare clean sugar processes with hydrolysates; test and scale fermentation to improve titer, rate, and yield; provide integrated, bench-scale data for TEA and LCA; scale fermentation to produce data for Learn.
- Task 5: Industry Engagement (Babs Marrone/Chris Johnson/Phil Laible co-leads)
 - Identify barriers to industry adoption of synthetic biology technologies, expand number and diversity of industry partnerships, and establish a set of metrics for determining impact of project technologies on industry.
- Task 6: Management (Blake Simmons lead)
 - Manage project management, develop internal and external communications, provide deliverables to BETO, and make some capital equipment purchases.





Project Management – Org Chart







Project Management – Roles and Responsibilities

Executive Committee

- Composition: representative from each Lab, PI, Program Manager, BETO Technology Manager, industry/management Task leads, others as needed
- Strategic direction and oversight
- Support collaboration between institutions
- ABF policy guidance
- Conflict resolution and performance management

Project Management and Integration Team

- Composition: Program Manager, Task (co-)leads, others as needed
- Progress tracking
- Target/Host selection
- Technical challenge identification/resolution

Agile BioFoundry Program Manager

- Alastair Robinson 50% effort
- Manage overall project
- Collaboration and progress tracking tools
- Ensure adequate communication between labs for integration of whole consortium
- Primary communications and operations point-of-contact
- BETO reporting





Project Management – Communications

ABF is an integrated, geographically distributed multi-Lab team

Effective communications are essential

Regular Internal Communications

- Bi-weekly Executive Committee meetings
- Bi-weekly ABF Task Lead meetings
- Weekly to monthly target/host pair meetings
- Weekly software infrastructure user meetings / webinars
- Monthly activity reports to BETO Technology Manager
- Monthly activity summary including DBTL cycle reports to BETO
- Monthly Industry Outreach and Engagement Task team meetings
- Quarterly progress / milestone completion reports to BETO
- Software infrastructure (e.g. ICE, DIVA, EDD, LabKey, AgileBioCyc, Jupyter, github/bitbucket, etc.)
- SharePoint file storage and sharing
- Annual Learn Summit
- Annual ABF Meeting

External Communications

- ABF website (agilebiofoundry.org)
- Social media (@agilebiofoundry)
- Presentations, posters, booths at domestic and international scientific / technical conferences
- Publications
- Quarterly Industry Advisory Board meetings and Industry Listening Days
- Semi-annual Global BioFoundry Alliance meetings (pending)





The ABF National Lab Network



Phil Laible, Thathiana Benavides, Peter Larsen



Dayna Daubaras



Taraka Dale, Babs Marrone



Nathan Hillson, Blake Simmons, Alastair Robinson, Katy Christiansen



Gregg Beckham,
Mary Biddy,
Christopher Johnson,
Davinia Salvachua



Adam Guss



Jon Magnuson, Kristin Burnum-Johnson



John Gladden, Anne Ruffing, Corey Hudson

Jay Fitzgerald and Kevin Craig





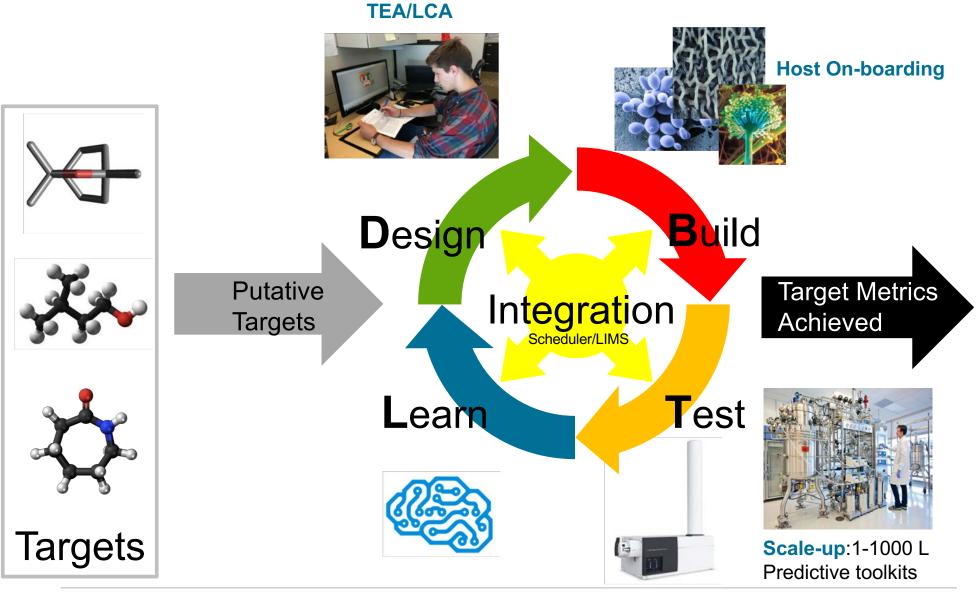


2 – Approach (Technical)





The Agile BioFoundry Approach







What makes ABF different than other BETOfunded metabolic engineering projects?

- The ABF has a variety of teams that work together in a highly collaborative fashion to:
 - Move target / host pairs through the pipeline
 - Build the tools and infrastructure to do so
 - More closely mirror industry in terms of breaking effort into domains (e.g. Test team)
- Learn component
- Infrastructure to support scale / throughput / depth of analysis / Learn
- Integrated whole that might be separated in other projects
 - Including Integrated Analysis (TEA/LCA), Host Onboarding, Scale-up





What is our plan to demonstrate these differences?

- Through our Presentations and Publications
 - See additional slides
- Peer Reviewer assessment of "unintuitive Learn TRY predictions"
 - Presented in subsequent Target/Host presentations
- Experimental assessment as to success rates for these TRY predictions
 - Presented in subsequent Target/Host presentations
- Scale up experiments designed to feed the Learn process
 - FY19 scale-up experiments include deep multi-omics analytics
- How we will ultimately leverage Learn for scale-up?
 - Future-looking perspective: science of scale-up in ABF out years FY20-22 and beyond





What are our Technical Risks and Mitigation Plans?

Risk	Severity	Description	Mitigation Plan
Designs do not work in selected host	Medium	Promoters / enzymes / pathways / etc. do not function as intended in the selected host.	Further test and learn from lack of function, and suggest design changes that could restore function
Lack of transferability of between target/hosts	Medium	Not able to leverage past efforts and learnings in one target-host pair for subsequent work in another	Further learn extents / likelihood of transferability
Infrastructure operating costs and value	Low	Costs of infrastructure (both hardware and software) maintenance and asset depreciation becomes unsustainable	Where possible, offload maintenance to more cost-effective and sustainable off-the-shelf vendor-supported solutions
Insufficient data to fully leverage Learn capabilities	Medium	Multi-omics datasets are not of the quality, quantity, or consistency needed for statistical analysis to identify engineering targets that lead to gains in titers, rates, and yields	Explicitly include Learn team Test data consumers during Design process to ensure Learn suitability of generated data





Definitions of ABF parlance / terms

Target / Host

- Target: the target molecule to be produced (e.g., adipic acid)
- Host: the microbial species hosting the metabolic pathway that produces the Target (e.g. P. putida)
- Target / Host pair: a Target paired with a specific Host to produce it
- Transfer Target: A Target the ABF has already produced in one Host, now paired with a new Host

DBTL vs mini-DBTL cycle

- DBTL cycle: complete Design / Build / Test / Learn engineering cycle, in which:
 - At least a minimum specified set of unit operations for each phase (e.g. at least targeted proteomics and metabolomics for Test) in the cycle has been completed
 - At least a minimum bandwidth / number of strain designs go into Build
 - At least a minimum fraction (but less than 100%) of these designed strains are built successfully
 - Resulting Test data set of requisite quantity, quality, reproducibility
 - Thresholds for minimum unit operations, quantities, quality, reproducibility are being standardized ABF-wide, keeping Learn requirements and opportunities foremost in mind
- mini-DBTL cycle: complete engineering cycle that does not meet all of the above criteria
 - Nonetheless, mini-DBTL cycles can result in useful actionable information
 - For example, a mini-DBTL cycle that only Tests for product titer or sugar consumption (but not full proteomics and metabolomics) can help prioritize candidates for a subsequent full DBTL cycle with deep multi-omics analysis
 - mini-DBTL cycles not meeting minimum Test unit operations can and should still be designed (and meet quantity / quality / consistency) to maximally leverage Learn.

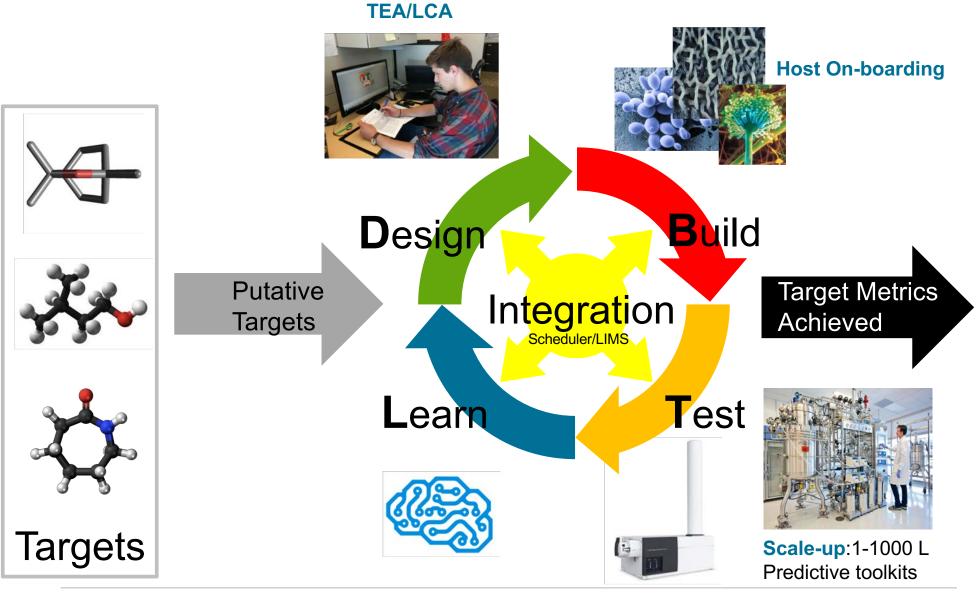




3 – Technical Accomplishments/ Progress/Results



Highlights from following ABF presentations





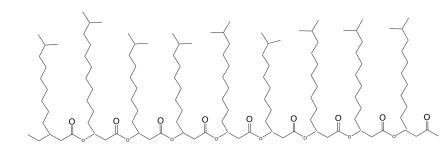


Highlights – P. putida

DBTL for Target 1: C6 diacids

- Baselining muconic acid production
- Improving rate of muconate production
- Successful Learn cycles for strain improvements

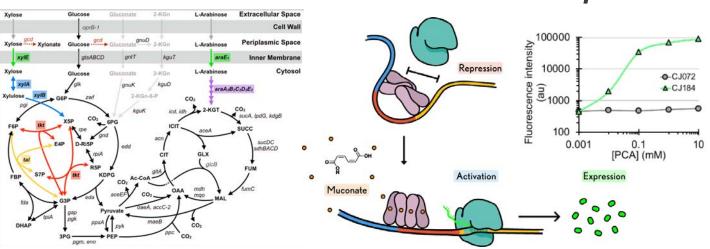




DBTL for Target 2: BCPHAs

New tools for P. putida

DBTL for sugar utilization



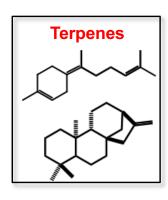


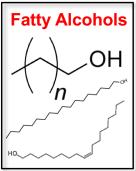


Highlights – R. toruloides

DBTL for Target 1: terpenes

- Baselining production of 4 terpenes
- Improving titers through MEV pathway optimization
- Successful Learn cycles for strain improvements





DBTL for Target 2: fatty alcohols

- Baselining production of FOH
- Improving titers through optimization of metabolite pools



Metabolic model

- Built a tailored model using omics,
 Tn-Seq, and Biolog data
- Used model to contextualize Learn data





Highlights – A. pseudoterreus

DBTL for Target 1: 3-hydroxypropionic acid

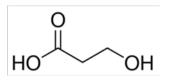
- Designed and Built pathway that achieved 2 g/L
- Improving TRY through multi-omics, FBA and ANN identified gene targets to increase biosynthesis of precursors and eliminate degradation of 3HP

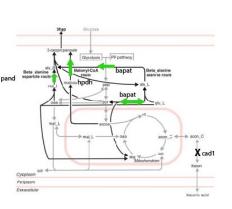
DBTL for Target 2: aconitic acid

- Achieved 12 g/L with initial strain
- Improving TRY by identifying and over-expressing mitochondrial and cell membrane transporters

Generally enabling learn applications

- Built a metabolic model and have used it to analyze multi-omics data and conduct genome-scale FBA, ID target fluxes
 - Used Artificial Neural Network approach to ID non-intuitive gene targets

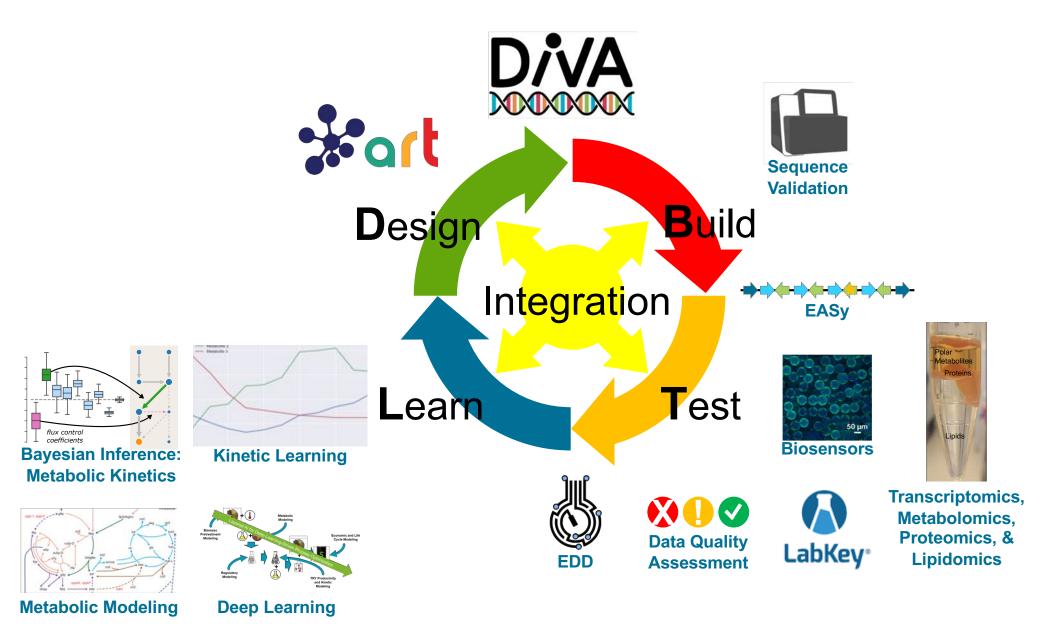








Highlights – DBTL infrastructure



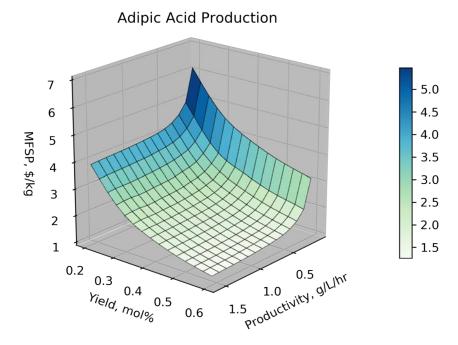




Highlights – Integrated Analysis

Example of outlining key drivers in both cost and sustainability

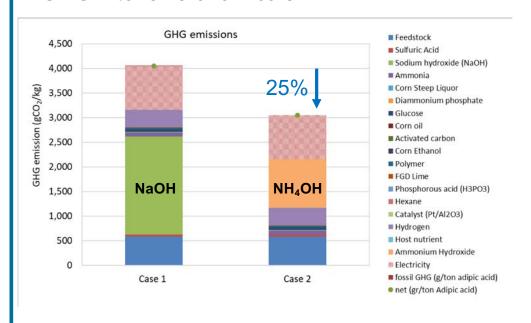
Quantify "economic gradient" of targeting yield or productivity



Key Outcome and Link to R&D:

Bounding analysis to show help identify critical R&D targets. ABF adopted 0.5 g/L/hr productivity target.

Decreasing GHG emission by using less GHG intensive chemicals



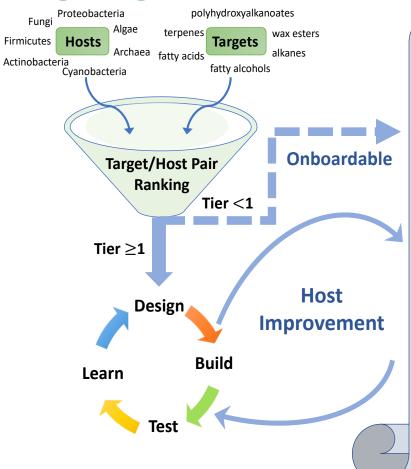
Key Outcome and Link to R&D:

ABF is testing the use of other neutralizing agents to see impact of performance.





Highlights – Host Onboarding



Tier System Criteria - "Hostability"

Tier 1

Annotated genome; growth conditions; growth kinetics and simple growth models; antibiotic susceptibility; selectable markers; transformation methods; plasmids/vectors; basic expression parts; biosafety/biosecurity information

Tier 2

Substrate utilization panel; toxicity profiles; bioreactor growth; counter-selectable markers; genome integration system; chromosomal safe sites/landing pads; induction systems; panel of constitutive promoters, RBSs, terminators; models of promoters and RBSs/Kozak sequences; genome-scale models; pan genome analysis; transcriptomic, proteomic, metabolomic datasets

Tier 3

Biosensors; cellular stress monitoring; CRISPR/CAS, Lambda Red, Cre-lox systems; advanced genomic integration platforms; gene expression tuning; high throughout protein engineering platform; lipidomic and glycomic datasets; centralized omics databases; multi-omic data integration and analysis; protein localization; protein degradation tags; protein interactome datasets; ¹³C-MFA experiments and model; kinetic model; population balance model

Tier 4

Culture scalability; saturated deletion/loss of function libraries; genomic overexpression platform; adaptive laboratory evolution/cell sorted libraries; baseline strains for maximal flux to metabolic nodes; cellular state sensors and dynamically regulated production strains; signaling model, gene regulation model, multi-scale model; predictive cellular model

- Tier 1 represents the basic tools needed for DBTL
- Hosts that do not meet Tier 1 require further development prior to usage
- Tools increase in sophistication as an organism moves up Tiers
- Not all tools in all Tiers are required for all organisms





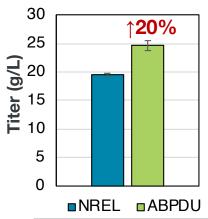
Highlights – Process Integration/Scale-up

Hydrolysate production

Two batches to date implementing process improvements at pilot scale

Pan-scale muconate Test/Learn



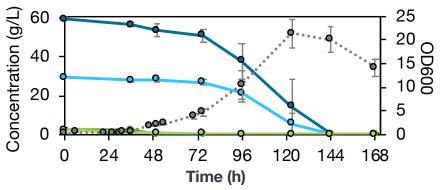


Round Robin study for muconate

4000 mL Out No 81000 318



Bioprocess development

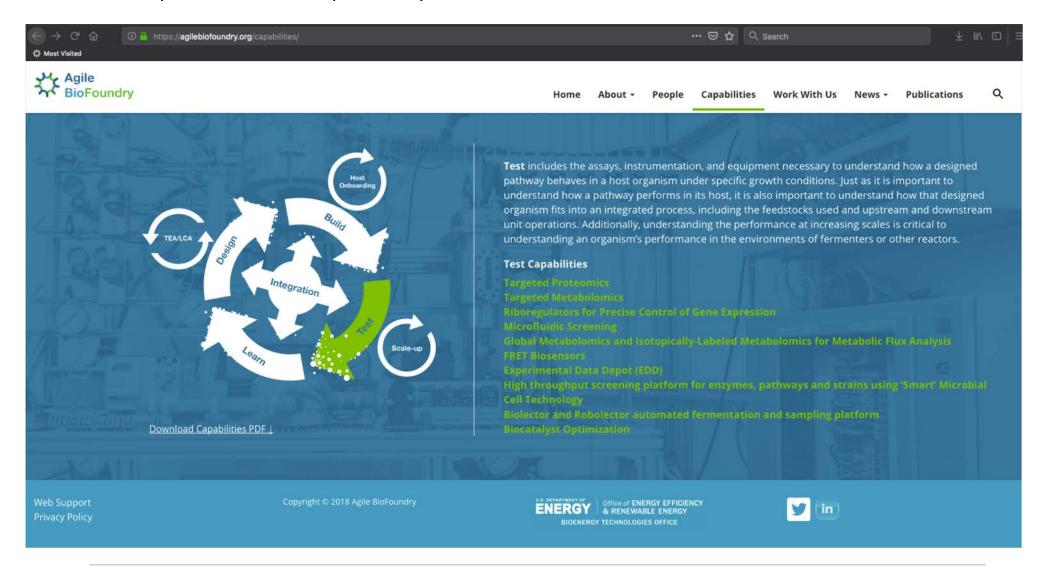






Highlights – Industry Outreach

- Revamped ABF website
 - Capabilities section improved in particular







Highlights – Management

- ABF Annual Meeting: September 10-12, 2018 in Emeryville, CA
 - Included public / open Industry Listening Day (with ABF Industry Advisory Board)





Target / Host selection process

- Subsequent ABF talks will present specifics of process implementation
 - For example, the Host Onboarding talk will discuss the quantitative assessment of "hostability"

• FY17

ABF identified 15 target / hosts for FY17-19, and prioritized three for FY17

• FY18

- ABF prioritized three additional targets (in existing hosts)
- Proactive feedback on prospective targets/hosts solicited from the ABF's Industry Advisory Board
- ABF direct-funded opportunity industry projects added additional targets / hosts

• FY19

- ABF prioritized one new target/host, and the transfer of three existing targets into different hosts
- BETO BEEPS FOA industry projects added additional targets / hosts
- BETO State of Technology (SOT) projects added additional hosts





FY17/18 Project Milestones Completed

Quarterly milestones and progress reporting, along with annual SMART milestones and Go/No-Go decisions

FY17 Annual SMART milestone

 Demonstrate the Agile BioFoundry process by successfully completing one or more Design, Build, Test, Learn cycles for 5 molecules in their designated onboarded hosts, hitting baseline titers of 100 mg/L in mock or DMR-EH hydrolysate for at least 2 molecules.

Go/No-Go Decision, Q2 FY18

 Demonstrate process integration and scaling in 2 L bioreactors in DMR-EH hydrolysate using a target molecule introduced into the BioFoundry in FY17 with a target titer of at least 1 g/L.

FY18 Annual SMART milestone

 From a set of 10 target molecules, demonstrate successful production of 40% with titers for FY18 target molecules of at least 100 mg/L in mock or DMR-EH hydrolysate, and titers for FY17 target molecules of at least 500 mg/L in DMR-EH hydrolysate.





FY19 Milestones Completed

Milestone (synopsis)	Task	FY19 Quarter	Туре
Selections of new target molecule & existing molecule in different host	Target/Host	Q1	Quarterly (Regular)
4X Build sequence validation capacity increase from FY18 to FY19	DBTL Infrastructure	Q2	Quarterly (Regular)
TEA and LCA on new FY19 target molecule	Integrated Analysis	Q2	Quarterly (Regular)
Deep Learning non-intuitive predictions	DBTL Infrastructure	Q2	Quarterly (Regular)
Titer goals in range of 1 to 10 g/L	Target/Host	Q3	Quarterly (Regular)
Transformation in new organism(s)	Host Onboarding	Q3	Quarterly (Regular)
5X Test capacity increase from FY17 to FY19	DBTL Infrastructure	Q3	Quarterly (Regular)
Promoters in new SOT organisms	Host Onboarding	Q4	Annual (Regular)
10L scale using DMR-EH hydrolysate, with 10 g/L, 100 mg/L/h, 40% yield	Process Integration & Scaling	Q4	Annual (Regular)
SWOT Analysis	Industry Engagement & Outreach	Q4	Annual (Regular)
DBTL Activity, Quarterly/Milestone, and final AOP reports sent to BETO. Updates to ABF website	Management	Q4	Annual (Regular)
Value of non-intuitive Learn predictions demonstrated	Target/Host	Q4	Go/No-Go





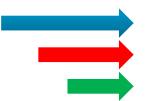
4 - Relevance



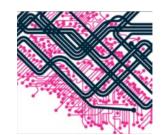


Relevant Outcomes

 50% reduction in time-to-scale up compared to the average of ~10 years



- 10X improvement in Design-Build-Test-Learn cycle efficiency
- Public infrastructure investment that increases U.S. industrial competitiveness and enables new opportunities for private sector growth and jobs



- New IP and manufacturing technologies effectively translated to U.S. industry ensuring market transformation
- New industrially relevant, optimized chassis organisms for fuel and chemical production







The Agile BioFoundry is complementary to BETO's other projects

- BETO's projects frequently target specific molecules/hosts
- In contrast, the Agile BioFoundry is a broadly enabling platform
 - Applicable across biorefinery fuel or chemical production processes
 - Other BETO projects could leverage Agile BioFoundry capabilities
 - Methods, workflows, instrumentation, software, expertise
 - Accumulated enzyme/pathway/host/process Learnings and data
- Agile BioFoundry development/assessment through several use cases
 - Sufficient number/diversity of molecules/hosts to demonstrate broad utility





Connections to other BETO projects

Other BETO consortia

- Continue to integrate TEA/LCA support across consortia
- Closer collaborations to further inform the DBTL cycle
- ChemCatBio: catalytically convert ABF molecules into value-added compounds
- SepCon: secreted hydrophobic, acid, and intracellular products recovery
- FCIC: understanding the effect of feedstock variability on strain robustness
- Performance-Advantaged BioProducts: ABF molecules could be used









BETO State Of Technology (SOT)

Improve genetic tools for SOT organisms to accelerate & increase DBTL cycle efficiency

Application of Energy I-Corp Learnings:

- Better Utilization of Real-time Data for in-line process Control
- Predictive Scale-Up studies in lab-scale bioreactors





ABF and other DOE programs

- Complementary ABF domain expertise, infrastructure, and operational TRL range offer opportunities for synergy with other DOE programs
- The ABF is open to working with other DOE funded projects and centers, such as the BRCs and EFRCs
 - Target/host suggestions for ABF
 - Scientists can propose biofuel and bioproduct targets for the ABF to work on and further optimize
 - Technology off-ramping into ABF
 - Early stage DBTL infrastructure (e.g. software, devices, methods) and microbial hosts can be brought into the ABF and further developed and operationalized
 - Shared technical challenges collaboratively addressed
 - Example: experiment data storage and dissemination EDD co-development
 - Resulting resources made accessible across projects P. putida mutant libraries
 - Provide compelling examples of DOE teams working together
 - Across TRLs and bridging the gap between fundamental and applied science and technology
 - Enhance technology transfer and commercialization efforts





Working with Industry: FY17 Direct-Funded Opportunities and FY18 BEEPS FOAs

Poster Session (Tuesday March 5)

Will include presentations on the ABF DFO projects (be sure not to miss them!)

Process and Management

Will be discussed in ABF Directed Funding Opportunities and Partnerships presentation

Why these projects and BETO investments are so important

- Expand the range of ABF targets and hosts
- Stress-test ABF capabilities and identify weaknesses and opportunities
- Bring new technologies in to the ABF and opportunities to license ABF technology out
- Early stage investments that will be crucial to the ABF accomplishing its overall goal and its desired outcomes (many relate directly to industry impact and technology transfer)
- Ensure that ABF development is responsive to industry
- Increase industry exposure (beyond funded companies) to the ABF and its capabilities
- Quantitatively demonstrate industry interest in leveraging the ABF

New for FY19: template ABF CRADA

- Publicly accessible from the ABF website: https://agilebiofoundry.org/work-with-us/
- Non-negotiable for projects receiving DOE funding
- Includes new "Extended Non-Exclusive Option" IP model





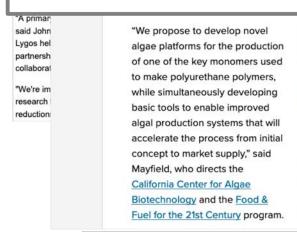
Relevance to Industry (in their own words)

CORRECTING and REPLACING – Lygos Partners with Agile BioFoundry and U.S. Department of Energy to Accelerate BioProduct R&D and Commercialization

Two-year, \$1.43 million pilot collaboration to automate microbial engineering research technology



"This grant is part of a significant new initiative by the Department of Energy and other agencies to support the 'bio-economy,' which is using living organisms to manufacture products," said Mayfield. "This is one of the fastest growing sectors for creating new jobs, as well as for developing new advanced materials and products."









5 – Future Work





How we are thinking about our future work

- We have a long term strategic vision for the ABF
- Our future work will focus on the technical and operational barriers to achieving the overall ABF goal and its desired outcomes
- Some challenges facing the ABF:
 - Show Learn can add value through non-intuitive predictions
 - Demonstrate industry-relevant ABF competencies across targets and hosts
 - Onboard new hosts and develop tools for them
 - Increase DBTL cycle capacities and efficiencies; reduce cycle time
 - Keep current strength / weakness / opportunities / threat (SWOT) assessments
 - Demonstrate reproducible geographically distributed unit operations
 - Find sustainable ABF IP / licensing / contracting model(s)
 - Demonstrate that past work and Learnings increase the efficiency of new work
- Next slides show our current FY19 and pending FY20-22 milestones
 - Subsequent ABF presentations provide additional examples of future work





FY19 Milestones To Be Completed

Milestone (synopsis)	Task	FY19 Quarter	Туре
Selections of new target molecule & existing molecule in different host	Target/Host	Q1	Quarterly (Regular)
4X Build sequence validation capacity increase from FY18 to FY19	DBTL Infrastructure	Q2	Quarterly (Regular)
TEA and LCA on new FY19 target molecule	Integrated Analysis	Q2	Quarterly (Regular)
Deep Learning non-intuitive predictions	DBTL Infrastructure	Q2	Quarterly (Regular)
Titer goals in range of 1 to 10 g/L	Target/Host	Q3	Quarterly (Regular)
Transformation in new organism(s)	Host Onboarding	Q3	Quarterly (Regular)
5X Test capacity increase from FY17 to FY19	DBTL Infrastructure	Q3	Quarterly (Regular)
Promoters in new SOT organisms	Host Onboarding	Q4	Annual (Regular)
10L scale using DMR-EH hydrolysate, with 10 g/L, 100 mg/L/h, 40% yield	Process Integration & Scaling	Q4	Annual (Regular)
SWOT Analysis	Industry Engagement & Outreach	Q4	Annual (Regular)
DBTL Activity, Quarterly/Milestone, and final AOP reports sent to BETO. Updates to ABF website	Management	Q4	Annual (Regular)
Value of non-intuitive Learn predictions demonstrated	Target/Host	Q4	Go/No-Go





Pending FY20-22 Milestones

We will put our plans into our FY20-22 AOP proposal.

The following milestones are proposed (will undergo merit review)

FY20 Annual Smart

 Reproducibility of 3 distributed Test unit operations including bioreactor scale-up quantified through comparison of results post data quality assurance for on-site vs. off-site sample analysis.

or,

 Statistics gathered and Industry partner decision making processes analyzed for choice between traditional (exclusive license, shorter option period) and alternative (non-exclusive, longer option period) CRADA IP model that retains incentives for industry yet enables ABF to learn and leverage past experience.

Go/No-Go Decision, Q2 FY21

 5 target molecules / tools transferred between host organisms and efficiency gains over prior host organisms assessed

FY22 Annual Smart

 5X efficiency improvement in DBTL engineering cycle demonstrated compared to FY19 baseline and 20 host organisms on-boarded to tier 1 or above





Summary

 Goal: Enable biorefineries to achieve 50% reductions in time to bioprocess scale-up as compared to the current average of around 10 years by establishing a distributed Agile BioFoundry that will productionize synthetic biology.



 Outcomes: 10X improvement in Design-Build-Test-Learn cycle efficiency, new host organisms, new IP and manufacturing technologies effectively translated to U.S. industry ensuring market transformation.



 Relevance: Public infrastructure investment that increases U.S. industrial competitiveness and enables new opportunities for private sector growth and jobs.







Acknowledgements

- Gregg Beckham
- Thathiana Benavides Gallego
- Mary Biddy
- Katy Christiansen
- Taraka Dale
- Dayna Daubaras
- Jay Fitzgerald
- Hector Garcia Martin
- John Gladden
- Adam Gus
- Christopher Johnson
- Robin Johnston
- Phil Laible
- Jon Magnuson
- Babs Marrone
- Todd Pray

- Alastair Robinson
- Davinia Salvachua
- Blake Simmons
- Deepti Tanjore





Additional Slides





Responses to Previous Reviewers' Comments

- Weaknesses include geographic separation
 - As a distributed effort, we clearly have faced operational challenges, although these have more than been made up for by the Agile BioFoundry's ability to leverage physical and human resources across distributed national laboratories. The Agile BioFoundry's program manager, together with regular communications across the consortium (via teleconferences, webinars, informatics servers, SharePoint, annual in-person meetings), have helped mitigate communications risks. Sample transfer risks (i.e., sample stability, sample loss) will continue to be assessed through local/proximal compared with remote sample analysis, and to date we have not suffered from any notable sample losses. We are continuing to make progress in addressing disconnects in technology adoption, and it continues to be an operational imperative to standardize workflows and data-exchange formats wherever possible.
- Do not yet have a compelling argument as to why and how their approach will be better than other potential approaches to the problem
 - What sets the Agile BioFoundry apart from other foundries is that we develop and distribute publicly available tools, methods, and strains aimed at broadly benefiting the biofuels and bioproducts industry. Whereas private foundries are incentivized to develop proprietary tools and organisms, the Agile BioFoundry is a publicly funded effort aimed at delivering technology that will enable industry to either leverage our resources through partnership or adopt our methodologies for developing bioproducts. In comparison to the publicly funded Defense Advanced Research Projects Agency Living Foundries program, there are distinct programmatic and technical differences between the aims of the two efforts. Where the Living Foundries program is primarily focused on developing biological pathways to materials that cannot be achieved through transformations of petroleum feedstocks, the Agile BioFoundry is focused developing biological pathways for producing advanced biofuels and renewable, high-volume chemicals.





Responses to Previous Reviewers' Comments (cont.)

- Rationale for their choice of product targets needs to be strengthened
 - The Agile BioFoundry is pursuing multiple target/hosts to demonstrate that the methods, software, and technologies can be productively applied across product classes. The process and rationale for selecting the three target/hosts pairs for FY 2017 (and the 15 pairs initially prioritized for FY 2017 FY 2019) was described during the 2017 Peer Review, and the details were provided to BETO. For our FY 2018 and FY 2019 target/host selection processes, in addition to quantitative technical assessments across multiple categories (TEA and Market, LCA, Strategic Value, Scientific Novelty, DOE Relevance, How Designable, How Buildable, How Hostable, How Testable, How Scalable, and Chemical and Biological Safety), we proactively consulted with the Agile BioFoundry Industry Advisory Board to ensure that our prioritized targets and hosts remain aligned with industry's needs.
- Isn't clear that reducing the cycle time to, say, adipic acid, would be generally applicable to other material
 - As will be / has been presented in the Target/Host ABF presentations at the 2019 Peer Review, we have started to diligently measure cycle times across targets and hosts. This is the pre-requisite step to measuring improvements in (i.e., reductions to) cycle time. It should be noted that we are now pursuing multiple targets in the same host (which could suggest how cycle times for the second target have benefitted from improvements for the first target) and the same target in multiple hosts (which could suggest how cycle times in the second host have benefitted from improvements for the first host). While the former is more directly relevant for this previous reviewer's comment, both are important to capture and understand as they both directly affect the Agile BioFoundry's ability to broadly accelerate biomanufacturing process development across targets and hosts.





Responses to Previous Reviewers' Comments (cont.)

- More emphasis should be placed on the performance gap between small-scale culturing and bench-scale fermentation, which is a well-known problem in the field
 - We recognize that there are challenges associated with each increase in process scale, including the transition from high-throughput, small-scale culturing to bench-scale fermentation. Agile BioFoundry workflows leverage design of experiments and small-scale culture to select strains to grow in bench-scale bioreactors. Bench-scale fermentation provides critical data for the "Learn" component of Design-Build-Test-Learn, both to inform future designs and to develop predictive models that may be applied to small-scale experiments. Agile BioFoundry facilities have recently procured Robo/Biolector(Pro) and Ambr250 instrumentation which both serve to bridge the gap between small-scale culturing and bench-scale fermentation.
- PI is encouraged to look deeply into high-throughput fermentation techniques mastered by enzymes and biobased chemicals and fuels companies
 - As mentioned above, towards adopting the techniques practiced and mastered by companies, Agile BioFoundry facilities have recently procured Robo/Biolector(Pro) and Ambr250 high-throughput fermentation instrumentation.
- Encourage the PI to form a strong liaison between fermentation and the highthroughput team
 - There are strong connections between Agile BioFoundry high-throughput and bio-reactor fermentation teams, with staff shared in common between them.





Publications

- Chen Y, Vu J, Thompson MG, Sharpless WA, Chan LJG, Gin JW, et al. (2019) A rapid methods development workflow for high-throughput quantitative proteomic applications. PLoS ONE 14(2): e0211582. https://doi.org/10.1371/journal.pone.0211582
- Garima Goyal, Zak Costello, Jorge Alonso Guitierrez, Aram Kang, Taek Soon Lee, Hector Garcia Martin, and Nathan J Hillson. (2018) "Parallel Integration and Chromosomal Expansion of Metabolic Pathways" ACS Synthetic Biology DOI: 10.1021/acssynbio.8b00243
- Costello, Zak, and Hector Garcia Martin. "A machine learning approach to predict metabolic pathway dynamics from time-series multiomics data." NPJ systems biology and applications 4.1 (2018): 19. https://doi.org/10.1038/s41540-018-0054-3
- Oyetunde, Tolutola, et al. "Leveraging knowledge engineering and machine learning for microbial bio-manufacturing." Biotechnology advances (2018). https://doi.org/10.1016/j.biotechadv.2018.04.008
- Amin Zargar, Jesus F. Barajas, Ravi Lal, Jay D. Kealsing. "Polyketide Synthases as a Platform for Chemical Product Design" AIChE (2018) https://doi.org/10.1002/aic.16351
- Jha RK*, Bingen JM, Johnson CW, Kern TL, Khanna P, Trettel DS, Straus CEM, Beckham GT, Dale T* (2018). A protocatechuate biosensor for Pseudomonas putida KT2440 via promoter and protein evolution. Metabolic Engineering Communications (6) 33-38. https://doi.org/10.1016/j.meteno.2018.03.001
- Mitchell G. Thompson, Nima Sedaghatian, Jesus F. Barajas, Maren Wehrs, Constance B. Bailey, Nurgul Kaplan, Nathan J. Hillson, Aindrila Mukhopadhyay & Jay D. Keasling. (2018) "Isolation and characterization of novel mutations in the pSC101 origin that increase copy number". Scientific Reports 8, 1590 doi:10.1038/s41598-018-20016-w
- Jesus F. Barajas, Amin Zargar, Bo Pang, Veronica T. Benites, Jennifer Gin, Edward E. K. Baidoo, Christopher J. Petzold, Nathan J. Hillson, and Jay D. Keasling. (2018) "Biochemical Characterization of β-Amino Acid Incorporation in Fluvirucin B2 Biosynthesis". ChemBioChem 10.1002/cbic.201800169
- Denby, Charles M., et al. "Industrial brewing yeast engineered for the production of primary flavor determinants in hopped beer." Nature communications 9.1 (2018): 965
- Garber ME, Rajeev, Kazakov AE, Trinh J, Masuno D, Thompson M, Kaplan, N, Novichkov PS and Mukhopadhyay A. (2018) "Multiple signaling systems target a core set of transition metal homeostasis genes using similar binding motifs" Mol Microbiol. 107(6):704-717. doi: 10.1111/mmi.13909
- Ando, D., Garcia Martin, H. (2018) "Two-Scale 13C Metabolic Flux Analysis for Metabolic Engineering". In "Synthetic Metabolic Pathways Methods and Protocols", Springer Protocols Methods in Molecular Biology, Jensen, Michael Krogh, Keasling, Jay D (Eds.) ISBN 978-1-4939-7295-1 http://www.springer.com/us/book/9781493972944
- Backman TWH, Ando D, Singh J, Keasling JD, García Martín H. (2018) "Constraining Genome-Scale Models to Represent the Bow Tie Structure of Metabolism for (13)C Metabolic Flux Analysis". Metabolites. 2018 Jan 4;8(1). pii: E3. doi: 10.3390/metabo8010003
- Yuzawa S, Bailey CB, Fujii T, Jocic R, Barajas JF, Benites VT, Baidoo EEK, Chen Y, Petzold CJ, Katz L, Keasling JD. Heterologous Gene Expression of N-Terminally Truncated Variants of LipPks1 Suggests a Functionally Critical Structural Motif in the N-terminus of Modular Polyketide Synthase.
 ACS Chem Biol. 2017 Nov 17;12(11):2725-2729. doi: 10.1021/acschembio.7b00714





Publications (cont.)

- Morrell, W., Birkel, G., Forrer, M.,; Lopez, T., Backman, T.W.H, Dussault, M., Petzold, C., Baidoo, E., Costello, Z., Ando, D., Alonso Gutierrez, J., George, K., Mukhopadhyay, A., Vaino, I., Keasling, J., Adams, P., Hillson, N., Garcia Martin, H. "The Experiment Data Depot: a web-based software tool for biological experimental data storage, sharing, and visualization" (2017) ACS Synthetic Biology DOI: 10.1021/acssynbio.7b00204
- Eng, C.H.*, Backman, T.W.H.*, Bailey, C.B., Magnan, C., Garcia Martin, H.G., Katz, L., Baldi, P., Keasling, J.D. "ClusterCAD: a computational platform for type I modular polyketide synthase design." (2017) Nucleic Acids Research DOI: 10.1093/nar/gkx893 *Contributed equally
- Barajas, J.F., Blake-Hedges, J., Bailey, C.B., Curran, S., Keasling, J.D. (2017). "Engineered polyketides: Synergy between protein and host level engineering" Synthetic and Systems Biotechnology doi.org/10.1016/j.synbio.2017.08.005
- Shymansky, Christopher M., et al. "Flux-enabled exploration of the role of Sip1 in galactose yeast metabolism." Frontiers in Bioengineering and Biotechnology 5 (2017)

Presentations

- Gregg Beckham, Hybrid biological and catalytic processes to manufacture and recycle plastics, Princeton University, November 28th, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". Ginkgo Bioworks, Boston, MA, November 12, 2018
- Nathan J. Hillson. "DIVA (DNA Design, Implementation, Validation Automation) Platform". Invited Talk, 2nd Darmstadt RoboWorkshop, Darmstadt, Germany, November 8, 2018
- Nathan J. Hillson. "Recent developments at the U.S Department of Energy Agile BioFoundry". Invited Talk, 2nd Darmstadt RoboWorkshop, Darmstadt, Germany, November 7, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". AIChE annual meeting, Pittsburgh, PA, October 31 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". Thermo Fisher, San Jose, CA, October 19, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". DTRA Tech Watch, Ft. Belvoir, VA, October 10, 2018
- Nathan J. Hillson. "DOE Agile BioFoundry Overview". Invited Talk, SynBioBeta 2018 visit to ESE, Emeryville, CA, October 1, 2018
- Nathan J. Hillson. "ABF Organization, Progress, and FY19 Plans". Invited Talk, ABF All Hands Annual Meeting 2018 (Industry Day), Emeryville, CA, September 12, 2018
- Nathan J. Hillson. "Agile BioFoundry Overview". Invited Talk, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018.
- Garcia Martin, H. "A new approach to flux analysis". Invited Talk, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018





Presentations (cont.)

- Hector Plahar. "DIVA Software Platform". Invited Talk, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Tijana Radivojevic. "Automatic Recommendation Tool", Invited Talk, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Jennifer Chiniquy. "DIVA DNA-Seq and DNA Construction", Invited Talk, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Garcia Martin, H. "A New Approach to Flux Analysis". ABF Annual Meeting, Berkeley CA, September 7, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". Invited talk, Machine learning for science workshop, Berkeley, CA, September 5, 2018
- Nathan J. Hillson. "Agile BioFoundry Overview". Invited Lightning Talk, LBNL BioSciences Area Retreat 2018, Lafayette, CA, August 30, 2018
- Garcia Martin, H. "Modeling from molecules to ecosystems: opportunities, challenges and vision". Invited talk, BioEpic meeting, Berkeley, CA, August 23, 2018
- Garima Goyal "DIVA DNA Construction". Invited Talk, JBEI Annual Meeting 2018, Sonoma, CA, August 20-22, 2018
- Tijana Radivojevic. "Automatic Recommendation Tool", Invited Talk, JBEI Annual Meeting 2018, Sonoma, CA, August 22, 2018
- Garcia Martin, H. "Opportunities in the intersection of synthetic biology, machine learning and automation". Invited talk, JBEI Annual Meeting, Berkeley, CA, August 20, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". Invited talk, SIMB, Chicago, IL, August 15, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". Invited talk, International Workshop for BioDesign and Automation (IWBDA), Berkeley, CA, August 2nd, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". Invited talk, Biocruces, Bilbao, Spain, July 20, 2018
- Garcia Martin, H. "Machine Learning to Predict Metabolic Pathway Dynamics from Multiomics Data". Invited talk, Al for synthetic biology, Stockholm, Sweden, July 15, 2018
- Garcia Martin, H. "Towards a predictive synthetic biology enabled by machine learning and automation". Invited talk, BCAM, Bilbao, Spain, July 3, 2018
- Nathan J. Hillson, "Berkeley (and other) National Lab(s): Current Biosecurity Frameworks and Strategies in Action", Invited Talk, EBRC meeting -Improving Security Considerations in Engineering Biology Research, Emeryville, CA, June 26, 2018
- Nathan J. Hillson and Hector A. Plahar, "ICE Software Platform", Invited Talk, Software for Synthetic Biology Workflows Workshop, SEED 2018, Scottsdale, Arizona, June 7, 2018
- Gregg Beckham. Developing new processes to valorize lignin and sugars to building-block chemicals and materials, RWTH Aachen University, May 28th, 2018





Presentations (cont.)

- Gregg Beckham. Adventures in engineering Pseudomonas putida for expanded substrate specificity and improved tolerance, RWTH Aachen University, May 28th, 2018
- Hillson, N.J. "Berkeley Lab project activities, biosecurity practices, and their roles within the larger biosecurity landscape". Invited Talk, Working Group on Automation in SynBio, Gryphon Scientific, Takoma Park, MD, May 23, 2018
- Hillson, N.J. "Recent developments at the Agile BioFoundry". Invited Talk, Diligence Ventures/Suzhou Government visit to ABF, Emeryville, CA, May 2, 2018
- Gregg Beckham. Hybrid biological and catalytic processes to manufacture and recycle plastics, MIT, April 27th, 2018
- Hillson, N.J. "Recent developments at the Agile BioFoundry". Invited Talk, 2018 Life Science Symposium Synthetic Biology and Metabolic Engineering, MilliporeSigma Innovation Center, St. Louis, MO, April 27, 2018
- Garcia Martin, H. " A Machine Learning Approach to Predict Metabolic Pathway Dynamics from Time Series Multiomics Data". Invited talk at Madison Microbiome Meeting at University of Wisconsin, Madison, WI, April 25, 2018.
- Jennifer Chiniquy, Cindi Hoover, Joel Guenther, Nurgul Kaplan, Garima Goyal, Mark Kulawik, Hector Plahar, Zachary Costello, Brian Bushnell, Samuel Deutsch, and Nathan J. Hillson. "Overcoming Challenges in MiSeq DNA Construct Sequence Validation". Invited Poster, DOE JGI User Meeting 2018, San Francisco, CA, March 14, 2018
- "Test" and "Learn" in process research informs design strategy Sundstrom, E. R.,, M. Mirsiaghi, F. Tachea, N. Sun, T.R. Pray, D. Tanjore. ECO-BIO, Dublin, Ireland, March 5, 2018.
- Garcia Martin, H. "EDD as a data warehouse and Learn facilitator". Invited talk at Argonne National Lab, St. Louis, Lemont, IL, March 5, 2018
- Garima Goyal, Nurgul Kaplan, Jennifer L. Chiniquy, Hector A. Plahar, Annabel Large, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "DIVA Services: PCR, Full DNA Construction, and MiSeq Validation". Invited Poster, DOE BER GSP Contractor's Meeting 2018, Tysons Corner, VA, February 27, 2018
- Hillson, N.J. "Three synthetic biology design challenges we face, and how we are approaching them". Invited Talk, Dagstuhl Seminar 18082, Wadern, Germany, February 19, 2018
- Jennifer Chiniquy, Nurgul Kaplan, Garima Goyal. "DIVA DNA-Seq Service", JBEI User Meeting presentation, February 12, 2018.
- Garcia Martin, H. "Metabolic Modeling of –omics Data for Biofuel Production". Invited talk at Bayer, Sacramento, CA, February 2, 2018.
- Garcia Martin, H. " Machine Learning and Mechanistic Models to Predict Biological Outcomes using 'omics Data". Invited talk at Environmental Genomics and Systems Biology retreat, Berkeley, CA, January 19, 2018
- Jesus F. Barajas. "Current progress towards engineered PKS lactam pathways". JBEI/BBD group meeting presentation, December 13, 2017
- Hillson, N.J. "Agile BioFoundry Overview". Invited Talk, iSynBio/SIAT visit to JGI, Walnut Creek, CA, December 9, 2017
- Jennifer Chiniquy, Nurgul Kaplan. "DIVA DNA-Seq Service". ESE User Meeting presentation, November 20, 2017





Presentations (cont.)

- Hillson, N.J. "Agile BioFoundry Overview". Invited Talk, Cargill visit to ESE, Emeryville, CA, November 17, 2017
- Hillson, N.J. "Flanking Homology DNA Assembly, Protocol Design Software, and Synthetic DNA". Invited Talk, Bitesize Bio Webinar, November 15, 2017
- Simmons, B.A. and Hillson, N.J. "The BioDefense Foundry". Invited Talk, DTRA Tech Watch Briefing, Springfield, VA, November 8, 2017
- Hillson, N.J. "Agile BioFoundry Overview". Invited Talk, University of Wyoming, Laramie, WY, November 3, 2017
- Hillson, N.J. "Parallel Integration and Chromosomal Expansion of Metabolic Pathways". Invited Talk, University of Wyoming, Laramie, WY, November 3, 2017
- Hillson, N.J. "Agile BioFoundry Overview". Invited Talk, Braskem Zoom Teleconference, November 1, 2017
- Hector Garcia Martin. "Modeling of -omics data for Biofuel Production through Synthetic Biology". EECE Department seminar, Washington University, St. Louis MO, October 20th, 2017
- Hillson, N.J. "Agile BioFoundry Overview". Invited Talk, ABLC Next Tour of ESE (ABF/ABPDU/JBEI), Emerville, CA, October 16, 2017
- Hillson, N.J. "Agile BioFoundry Overview". Invited Talk, Berkeley Lab Workshop: Industrialization of engineering biology: from discovery to scale-up, SynBioBeta SF 2017, UCSF Mission Bay, San Francisco, CA, October 3, 2017
- Hillson, N.J. "How the Agile BioFoundry Thinks About Paths to Commercialization". Invited Talk, SynBio for Defense, Arlington, VA, September 27, 2017
- Hillson, N.J. "BioDefense the Agile BioFoundry and Predictive Biology". Invited Talk, Presentation for Dimitri Kusnezov (Chief Scientist, DOE NNSA), Berkeley, CA, September 21, 2017
- Hillson, N.J. "Sustainable development through a synthetic biology foundry". Invited Talk, CellPress LabLinks Basic to Applied Science for Sustainable Development, Berkeley, CA, September 18, 2017
- Plahar, H.A. "Software Session: Recent DeviceEditorjs/DIVA/ICE improvements". Invited Talk, JBEI Annual Meeting, Monterey, CA, September 15, 2017
- Costello, Z. "Software Session: The Automatic Recommendation Tool". Invited Talk, JBEI Annual Meeting, Monterey, CA, September 15, 2017
- Backman, T.W.H. "ClusterCAD: a computational platform for type I modular polyketide synthase design." Invited Talk, JBEI Annual Meeting, Monterey, CA, September 14, 2017
- Hillson, N.J. "Agile BioFoundry Update". Invited Talk, JBEI Annual Meeting, Monterey, CA, September 13, 2017
- Plahar, H.A. "ICE/DIVA Software Tutorial". Invited Talk, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 29, 2017
- Hillson, N.J. "Agile BioFoundry Overview". Invited Talk, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017
- De Paoli, H.C. "A. pseudoterreus 3HP Design and Build". Invited Talk, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017.
- Chiniquy J., "DIVA DNA-Seq Service". Invited Talk, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017





Presentations (cont.)

- Garcia Martin, H. "Predicting Metabolic Pathway Dynamics by Combining Multiomics Data with Machine Learning and Kinetic Modeling". Invited talk at "Multi-omics for Microbiomes" conference, Pasco, WA, July 31, 2017.
- Johnson, C.W. "Metabolic engineering of Pseudomonas putida KT2440 for production of muconic acid from sugar", SIMB Annual Meeting, July 31, 2017
- Hillson, N.J. "j5 Software Through the Years: Insights from Aggregate Public Usage Metrics". Invited lightning talk, World Metrology Day Symposium, Stanford, CA, May 22, 2017.
- Beckham, G.T. "The Agile BioFoundry: Investing in Biomanufacturing Infrastructure", TechConnect World, May 16, 2017
- Derek Vardon. Potential commercialization opportunities for valorization of biomass to polymer precursors. Invited Seminar. Alliance Commercialization and Deployment Committee Meeting, NREL. May 2017.
- Gregg Beckham. The Agile BioFoundry: Investing in Biomanufacturing Infrastructure, TechConnect World, May 16, 2017
- Hillson, N.J. "Overview of the Agile BioFoundry". Invited talk, IMP (Mexican Petroleum Institute) Visit to JBEI, Emeryville, CA, April 21, 2017.

Posters

- J. Meadows, C. Johnson, S. Notonier, YM. Kim, S.Tripathy, K. Burnam-Johnson, M. Burnet, J. Magnuson, G. Beckham, N. Hillson, J. Gladden. "Engineering Pseudomonas putida KT2440 to produce adipic acid from lignocellulosic components". Invited Poster, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Jesus F. Barajas, Jingwei Zhang, Amin Zargar, Bo Pang, Huaxiang Deng, Veronica T. Benites, Edward E. K. Baidoo, Christopher J. Petzold, Nathan J. Hillson, Jay D. Keasling. "Development of Valerolactam and Caprolactam Biosynthetic Routes". Invited Poster, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Garima Goyal, Nurgul Kaplan, Jennifer L. Chiniquy, Jonathan Diab, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Manjiri Tapaswi, Nina Stawski, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "DIVA (Design Implementation Validation Automation) DNA Construction". Invited Poster, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Jonathan Diab, Jennifer Chiniquy, Cindi Hoover, Joel Guenther, Nurgul Kaplan, Garima Goyal, Mark Kulawik, Hector Plahar, Zachary Costello, Brian Bushnell, Samuel Deutsch, and Nathan J. Hillson. "MiSeq DNA Construct Sequence Validation". Invited Poster, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Edward E.E.K. Baidoo and Veronica Teixeira Benites. "High throughput analysis of isoprenoid pathway intermediates by HILIC-QTOF-MS". Invited Poster, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018.
- Isaac Wolf, Carolina Barcelos, Shawn Chang, Nilufer Oguz, Matt Dorsey, Davinia Salvachua, Robert Nelson, Todd Pray, Eric Sundstrom and Deepti Tanjore. "Harmonization of Fermentation for Production of P. putida-derived Muconic Acid". Invited Poster, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018





Posters (cont.)

- J. Prahl, S. Coradetti, D. Liu, G. Geiselman, T. Pray, J. Gladden, E. Sundstrom, and D. Tanjore. "Insights from Bioreactors make Scale-Down Modeling more Effective". Invited Poster, ABF All Hands Annual Meeting 2018, Emeryville, CA, September 10, 2018
- Garima Goyal, Nurgul Kaplan, Jennifer L. Chiniquy, Jonathan Diab, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Manjiri Tapaswi, Nina Stawski, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "DIVA (Design Implementation Validation Automation) DNA Construction". Invited Poster, JBEI Annual Meeting 2018, Sonoma, CA, August 20-22, 2018
- William Morrell, Mark Forrer, Garrett Birkel, Traci Lopez, Nathan J Hillson, Hector Garcia Martin. "Collaboration with the Experiment Data Depot".
 Invited Poster, JBEI Annual Meeting 2018, Sonoma, CA, August 20-22, 2018
- Jonathan Diab, Jennifer Chiniquy, Cindi Hoover, Joel Guenther, Nurgul Kaplan, Garima Goyal, Mark Kulawik, Hector Plahar, Zachary Costello, Brian Bushnell, Samuel Deutsch, and Nathan J. Hillson. "MiSeq DNA Construct Sequence Validation". Invited Poster, JBEI Annual Meeting 2018, Sonoma, CA, August 20-22, 2018
- Sarah A LaFrance, Jacob Coble, Thomas Rich, Hector Plahar, Joshua Nixon, Nathan J. Hillson. "VectorEditor: Freely Open-Source Javascript Webapp for DNA Visualization, Annotation, and Editing". Invited Poster, JBEI Annual Meeting, Monterey, CA, September 13, 2017
- Annabel Large, Nurgul Kaplan, Jennifer Chiniquy, Garima Goyal, and Nathan Hillson. "Expansion and Optimization of DIVA DNA Sequence Validation Services". Invited Poster, JBEI Annual Meeting, Monterey, CA, September 13, 2017
- Garima Goyal, Nurgul Kaplan, Jennifer L. Chiniquy, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Manjiri Tapaswi, Nina Stawski, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "DIVA (Design Implementation Validation and Automation) DNA Construction". Invited Poster, JBEI Annual Meeting, Monterey, CA, September 13, 2017
- Nurgul Kaplan, Garima Goyal, Jennifer L. Chiniquy, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Manjiri Tapaswi, Nina Stawski, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "Using DIVA, DeviceEditor, and j5 for DNA Construction". Invited Poster, JBEI Annual Meeting, Monterey, CA, September 13, 2017
- William Morrell, Garrett Birkel, Mark Forrer, Traci Lopez, Nathan J Hillson, Hector Garcia Martin. "The Experiment Data Depot platform". Invited Poster, JBEI Annual Meeting, Monterey, CA, September 13, 2017
- Backman, T.W.H., Eng, C.H., Bailey, C.B., Keasling, J.D., Garcia Martin, H. "Software for polyketide synthase (PKS) design". Invited Poster, JBEI Annual Meeting, Monterey, CA, September 13, 2017
- Garima Goyal, Nurgul Kaplan, Jennifer L. Chiniquy, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Manjiri Tapaswi, Nina Stawski, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "DIVA (Design Implementation Validation and Automation) DNA Construction". Invited Poster, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017
- Nurgul Kaplan, Garima Goyal, Jennifer L. Chiniquy, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Manjiri Tapaswi, Nina Stawski, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "Using DIVA, DeviceEditor, and j5 for DNA Construction". Invited Poster, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017





Posters (cont.)

- Jennifer L. Chiniquy, Cindi A. Hoover, Joel M. Guenther, Nurgul Kaplan, Christopher W. Beitel, Samuel Deutsch, and Nathan J. Hillson. "Towards a High-Throughput Low-Cost Automated DNA Sequence Validation Workflow". Invited Poster, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017
- William Morrell, Garrett Birkel, Mark Forrer, Traci Lopez, Nathan J Hillson, Hector Garcia Martin. "The Experiment Data Depot platform". Invited Poster, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017
- Hector A. Plahar, Elena Aravina, Oge Nnadi, Joanna Chen, Paul D. Adams, Jay D. Keasling, and Nathan J. Hillson. "ICE: A Distributed and Interconnected Biological Part Registry". Invited Poster, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017
- Jha, R., Narayanan, N., Johnson, C., Beckham, G., Dale, T. "Whole cell biosensing in Pseudomonas putida KT2440". Invited Poster, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017
- Pandey N., Krishnamurthy, M., Jha, Ramesh., Hennelly, S., Dale, T. "Riboregulator Development To Increase Metabolic Flux Towards Muconate Production". Invited Poster, Agile BioFoundry Annual Meeting, NREL IBRF, Golden, CO, August 28, 2017
- John Meng, Angela Tarver, Matthew Hamilton, Robert Evans, Lisa Simirenko, Nathan J. Hillson, Jan-Fang Cheng, and Samuel Deutsch. "SynTrack 2:
 A Scalable DNA Assembly Production Workflow Management". Invited Poster, 2017 Synthetic Biology: Engineering, Evolution & Design (SEED),
 Vancouver, British Columbia, Canada, June 20-23, 2017.
- Sarah A LaFrance, Jacob Coble, Thomas Rich, Hector Plahar, Joshua Nixon, Nathan J. Hillson. "VectorEditor: Freely Open-Source Javascript Webapp for DNA Visualization, Annotation, and Editing". Invited Poster, 2017 Synthetic Biology: Engineering, Evolution & Design (SEED), Vancouver, British Columbia, Canada, June 20-23, 2017.
- William Morrell, Garrett Birkel, Mark Forrer, Traci Lopez, Nathan J Hillson, Hector Garcia Martin. "The Experiment Data Depot platform". Invited Poster, 2017 Synthetic Biology: Engineering, Evolution & Design (SEED), Vancouver, British Columbia, Canada, June 20-23, 2017.
- Nurgul Kaplan, Garima Goyal, Jennifer L. Chiniquy, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Nina Stawski, Manjiri Tapaswi, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "DIVA (Design, Implementation, Validation Automation) DNA Construction: Wet-Lab Workflow and Software Platform". Invited Poster, 2017 Synthetic Biology: Engineering, Evolution & Design (SEED), Vancouver, British Columbia, Canada, June 20-23, 2017.
- Philip C. Gach, Manasi Raje, Nurgul Kaplan, Sangeeta Nath, Samuel Deutsch, Jay D. Keasling, Paul D. Adams, Nathan J. Hillson and Anup K. Singh.
 "A Microfluidic Platform for Combinatorial Gene Assembly, Transformation, Culture and Assay". Invited Poster, 2017 Synthetic Biology: Engineering, Evolution & Design (SEED), Vancouver, British Columbia, Canada, June 20-23, 2017.
- Hillson, N.J. "j5 Software Through the Years: Insights from Aggregate Public Usage Metrics". Invited Poster, World Metrology Day Symposium, Stanford, CA, May 22, 2017.
- Jennifer L. Chiniquy, Cindi A. Hoover, Joel M. Guenther, Nurgul Kaplan, Christopher W. Beitel, Samuel Deutsch, and Nathan J. Hillson. "Towards a High-Throughput Low-Cost Automated DNA Sequence Validation Workflow". Invited Poster, World Metrology Day Symposium, Stanford, CA, May 22, 2017.





Posters (cont.)

- G. Goyal, Z. Costello, J.A. Gutierrez, A. Kang, T.S. Lee, H.G. Martin, and N.J. Hillson. "PIACE: Parallel Integration and Chromosomal Expansion of Biofuel Pathways in E. coli". Invited Poster, World Metrology Day Symposium, Stanford, CA, May 22, 2017.
- Nurgul Kaplan, Garima Goyal, Jennifer L. Chiniquy, Joel M. Guenther, Hector A. Plahar, Joanna Chen, Nina Stawski, Manjiri Tapaswi, Lisa Simirenko, Samuel Deutsch, and Nathan J. Hillson. "DIVA (Design, Implementation, Validation Automation) DNA Construction: Wet-Lab Workflow and Software Platform". Invited Poster, World Metrology Day Symposium, Stanford, CA, May 22, 2017.



